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Adler, Jon Elliot
Lindemeier, Juergen
The Regents of the University of California

<120> Assays for Sensory Modulators Using a Sensory Cell
Specific G-Protein Beta Subunit

<130> 02307E-092710US

<140> US 09/492,029
<141> 2000-01-26

<150> US 60/117,404
<151> 1999-01-27

<160> 5
<170> PatentIn Ver. 2.1

<210> 1
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<212> DNA
<213> Rattus sp.

<220>
<223> rat tongue circumvallate papillae taste receptor
cell cDNA clone 165-17

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agtcatgggc tgagcgctct ggccattccc argccggaca aaggctgctg gtagcccagg 120
agtcatctag ggtggggagg gtctgttctt gtttat 156

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<213> Rattus sp.

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<221> CDS
<222> (78)..(2000)
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(TC-Gbeta3)

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cccttgacct gtgaacc atg ggg gag atg gag cag ctg aag cag gag gcg 110
Met Gly Glu Met Glu Gln Leu Lys Gln Glu Ala .
1 5 10

gag cag ctc aag aag cag att gct gat gcc agg aaa gcc tgt gcg gac 158
Glu Gln Leu Lys Lys Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp
15 20 25

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atc act ctg gct gag ctt gtg tct ggc ctg gag gtg gtg gga cga gtc 206
Ile Thr Leu Ala Glu Leu Val Ser Gly Leu Glu Val Val Gly Arg Val
 30 35 40

cag atg cg^a aca cg^b agg acg tta agg gga cac ctg gct aag atc tat 254
Gln Met Arg Thr Arg Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr
 45 50 55

gcc atg cac tgg gcc act gac tct aag ctg cta gta agt gcc tcg cag 302
Ala Met His Trp Ala Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln
 60 65 70 75

gat ggg aag ctg atc gtg tgg gac act tac acc acc aat aag gtg cat 350
Asp Gly Lys Leu Ile Val Trp Asp Thr Tyr Thr Thr Asn Lys Val His
 80 85 90

gct atc ccg ctg cgt tcc tcc tgg gtc atg acc tgt gcc tat gca cca 398
Ala Ile Pro Leu Arg Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro
 95 100 105

tca ggg aac ttc gtg gca tgt ggg ggg cta gat aac atg tgc tca atc 446
Ser Gly Asn Phe Val Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile
 110 115 120

tac agc ctc aaa tcc cgt gag ggc aat gtc aag gtc agc cg^c gaa ctc 494
Tyr Ser Leu Lys Ser Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu
 125 130 135

tcg gct cac aca ggt tat ctc tcc tgt tgc cgc ttc ctg gat gac aac 542
Ser Ala His Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn
 140 145 150 155

aac att gtg act agc tct ggg gac acc acg tgt gcc ttg tgg gac att 590
Asn Ile Val Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile
 160 165 170

gag acg ggg cag cag aag aca gtg ttc gtg gga cac act ggt gac tgc 638
Glu Thr Gly Gln Gln Lys Thr Val Phe Val Gly His Thr Gly Asp Cys
 175 180 185

atg agc ctg gct gtg tcc cca gac tac aaa ctc ttc atc tcg gga gct 686
Met Ser Leu Ala Val Ser Pro Asp Tyr Lys Leu Phe Ile Ser Gly Ala
 190 195 200

tgt gat gcc agc gcc aag ctc tgg gat gtg agg gaa ggg acc tgt cgc 734
Cys Asp Ala Ser Ala Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg
 205 210 215

cag act ttc act ggc cac gag tca gac atc aat gct atc tgt ttc ttt 782
Gln Thr Phe Thr Gly His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe
 220 225 230 235

ccc aat ggg gag gcc atc tgc act ggc tca gat gat gcc tcc tgc cgc 830
Pro Asn Gly Glu Ala Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg
 240 245 250

ctc ttt gac ctg agg gca gac cag gaa ctg aca gcc tac tcc cac gag 878
Leu Phe Asp Leu Arg Ala Asp Gln Glu Leu Thr Ala Tyr Ser His Glu
 255 260 265

agc atc atc tgt ggc atc acg tcc gta gcc ttc tca ctc agt ggt cgc	926
Ser Ile Ile Cys Gly Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg	
270 275 280	
ctg ctc ttt gct ggc tat gat gac ttc aac tgc aat gtc tgg gac tct	974
Leu Leu Phe Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser	
285 290 295	
ctg aag tgt gag cgt gta ggc gtt ctt tct ggc cat gac aac aga gtc	1022
Leu Lys Cys Glu Arg Val Gly Val Leu Ser Gly His Asp Asn Arg Val	
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agt tgc ctg ggg gtc aca gct gac ggc atg gct gtg gcc act gga tcc	1070
Ser Cys Leu Gly Val Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser	
320 325 330	
tgg gac agc ttc ctc aag atc tgg aac tgaggaggct ggaggaagag	1117
Trp Asp Ser Phe Leu Lys Ile Trp Asn	
335 340	
gtggaaagcc atgaaggctc tcagctgact cctatgccct gtctccttag ggtcagtctt	1177
ctataccctg gggccactcc cagtaaactt ccttctaagg gcaggtggga ttataggagt	1237
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tagatgactc ctgggctacc agcagcggtt gtccggcctg ggaatggcca gagcgctcag	1417
cccatgacta tagtgtcac tccttagtac ctggctccct cccagcgact ttctttctgc	1477
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 <213> Rattus sp.

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35 40 45	
Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Ala	
50 55 60	
Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile	
65 70 75 80	
Val Trp Asp Thr Tyr Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg	
85 90 95	
Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Phe Val	
100 105 110	

Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Ser Leu Lys Ser
 115 120 125
 Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His Thr Gly
 130 135 140
 Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val Thr Ser
 145 150 155 160
 Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln
 165 170 175
 Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu Ala Val
 180 185 190
 Ser Pro Asp Tyr Lys Leu Phe Ile Ser Gly Ala Cys Asp Ala Ser Ala
 195 200 205
 Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe Thr Gly
 210 215 220
 His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly Glu Ala
 225 230 235 240
 Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp Leu Arg
 245 250 255
 Ala Asp Gln Glu Leu Thr Ala Tyr Ser His Glu Ser Ile Ile Cys Gly
 260 265 270
 Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg Leu Leu Phe Ala Gly
 275 280 285
 Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser Leu Lys Cys Glu Arg
 290 295 300
 Val Gly Val Leu Ser Gly His Asp Asn Arg Val Ser Cys Leu Gly Val
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 325 330 335
 Lys Ile Trp Asn
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A
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 <211> 1523
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (7)..(1029)
 <223> human taste cell specific G-protein beta 3 subunit

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Lys Lys Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Val Thr Leu		
15 20 25 30		
gca gag ctg gtg tct ggc cta gag gtg gtg gga cga gtc cag atg cgg		144
Ala Glu Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg		
35 40 45		
acg cgg cgg acg tta agg gga cac ctg gcc aag att tac gcc atg cac		192
Thr Arg Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His		
50 55 60		
tgg gcc act gat tct aag ctg ctg gta agt gcc tcg caa gat ggg aag		240
Trp Ala Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys		
65 70 75		
ctg atc gtg tgg gac agc tac acc acc aac gtc cac gcc atc cca		288
Leu Ile Val Trp Asp Ser Tyr Thr Asn Lys Val His Ala Ile Pro		
80 85 90		
ctg cgc tcc tcc tgg gtc atg acc tgc tat gcc cca tca ggg aac		336
Leu Arg Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn		
95 100 105 110		
ttt gtg gca tgt ggg ggg ctg gac aac atg tgt tcc atc tac aac ctc		384
Phe Val Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Asn Leu		
115 120 125		
aaa tcc cgt gag ggc aat gtc aag gtc agc cgg gag ctt tct gct cac		432
Lys Ser Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His		
130 135 140		
aca ggt tat ctc tcc tgc tgc cgc ttc ctg gat gac aac aat att gtg		480
Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val		
145 150 155		
acc agc tcg ggg gac acc acg tgc ttg tgg gac att gag act ggg		528
Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly		
160 165 170		
cag cag aag act gta ttt gtg gga cac acg ggt gac tgc atg agc ctg		576
Gln Gln Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu		
175 180 185 190		
gct gtg tct cct gac ttc aat ctc ttc att tcg ggg gcc tgt gat gcc		624
Ala Val Ser Pro Asp Phe Asn Leu Phe Ile Ser Gly Ala Cys Asp Ala		
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agt gcc aag ctc tgg gat gtg cga gag ggg acc tgc cgt cag act ttc		672
Ser Ala Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe		
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act ggc cac gag tcg gac atc aac gcc atc tgt ttc ttc ccc aat gga		720
Thr Gly His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly		
225 230 235		
gag gcc atc tgc acg ggc tcg gat gac gct tcc tgc cgc ttg ttt gac		768
Glu Ala Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp		
240 245 250		

A
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260																
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Cys	Gly	Ile	Thr	Ser	Val	Ala	Phe	Ser	Leu	Ser	Gly	Arg	Leu	Leu	Phe	
275															285	
280																
gct	ggc	tac	gac	tcc	aac	tgc	aat	gtc	tgg	gac	tcc	atg	aag	tct	912	
Ala	Gly	Tyr	Asp	Asp	Phe	Asn	Cys	Asn	Val	Trp	Asp	Ser	Met	Lys	Ser	
290															300	
295																
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Glu	Arg	Val	Gly	Ile	Leu	Ser	Gly	His	Asp	Asn	Arg	Val	Ser	Cys	Leu	
305															315	
310																
gga	gtc	aca	gct	gac	ggg	atg	gct	gtg	gcc	aca	ggt	tcc	tgg	gac	agc	1008
Gly	Val	Thr	Ala	Asp	Gly	Met	Ala	Val	Ala	Thr	Gly	Ser	Trp	Asp	Ser	
320															330	
325																
ttc	ctc	aaa	atc	tgg	aac	tgaggaggct	ggagaaagggg	aagtggagg								1056
Phe	Leu	Lys	Ile	Trp	Asn											
335																
340																
cagtgaacac	actcagcagc	cccctgcccc	accatatctc	attcagggtgt	tcttttat											1116
attccgggtg	ccattccac	taagcttct	ccttgaggg	cagtggggag	catgggactg											1176
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ccccagagcc	actaccttg	tccaggcctg	ggtggatag	ggcggttggc	cctgtgacta											1416
tggctctggc	accactaggg	tcctggccct	cttcttattc	atgcttctc	ctttttctac											1476
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<211> 340

<212> PRT

<213> Homo sapiens

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35 40 45

Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Ala
50 55 60

Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile
65 70 75 80

Val Trp Asp Ser Tyr Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg
85 90 95

Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Phe Val
100 105 110

Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Asn Leu Lys Ser
115 120 125

Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His Thr Gly
130 135 140

Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val Thr Ser
145 150 155 160

Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln
165 170 175

Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu Ala Val
180 185 190

Ser Pro Asp Phe Asn Leu Phe Ile Ser Gly Ala Cys Asp Ala Ser Ala
195 200 205

Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe Thr Gly
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His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly Glu Ala
225 230 235 240

Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp Leu Arg
245 250 255

Ala Asp Gln Glu Leu Ile Cys Phe Ser His Glu Ser Ile Ile Cys Gly
260 265 270

Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg Leu Leu Phe Ala Gly
275 280 285

Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser Met Lys Ser Glu Arg
290 295 300

Val Gly Ile Leu Ser Gly His Asp Asn Arg Val Ser Cys Leu Gly Val
305 310 315 320

Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser Phe Leu
325 330 335

Lys Ile Trp Asn
340